

SEQUENCE LISTING

<110> Mack, David
Gish, Kurt
Wilson, Keith

<120> NOVEL METHODS OF DIAGNOSING CANCER, COMPOSITIONS, AND METHODS OF SCREENING FOR CANCER MODULATORS

<130> A-69192-1/DJB/JJD/AMS

<150> US 09/608,821

<151> 2000-06-30

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<170> PatentIn version 3.0

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Ile Leu Asp Arg Leu Arg Pro Asn Ile Ile Pro Val Leu Asp Glu Ile	
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aag tcc atg gca aca gcg atc aag gag acc aaa gag gcg ttg gag aac	823
Lys Ser Met Ala Thr Ala Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn	
250 255 260	
atg aac agc acc ttg aag agc ttg cac caa caa agt aca cag ctt agc	871
Met Asn Ser Thr Leu Lys Ser Leu His Gln Gln Ser Thr Gln Leu Ser	
265 270 275	
agc agt ctg acc agc gtg aaa act agc ctg cgg tca tct ctc aat gac	919
Ser Ser Leu Thr Ser Val Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp	
280 285 290	
cct ctg tgc ttg gtg cat cca tca agt gaa acc tgc aac agc atc aga	967
Pro Leu Cys Leu Val His Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg	
295 300 305 310	
ttg tct cta agc cag ctg aat agc aac cct gaa ctg agg cag ctt cca	1015
Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro	
315 320 325	

ccc gtg gat gca gaa ctt gac aac gtt aat aac gtt ctt agg aca gat	1063
Pro Val Asp Ala Glu Leu Asp Asn Val Asn Asn Val Leu Arg Thr Asp	
330 335 340	
ttg gat ggc ctg gtc caa cag ggc tat caa tcc ctt aat gat ata cct	1111
Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro	
345 350 355	
gac aga gta caa cgc caa acc acg act gtc gta gca ggt atc aaa agg	1159
Asp Arg Val Gln Arg Gln Thr Thr Val Val Ala Gly Ile Lys Arg	
360 365 370	
gtc ttg aat tcc att ggt tca gat atc gac aat gta act cag cgt ctt	1207
Val Leu Asn Ser Ile Gly Ser Asp Ile Asp Asn Val Thr Gln Arg Leu	
375 380 385 390	
cct att cag gat ata ctc tca gca ttc tct gtt tat gtt aat aac act	1255
Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser Val Tyr Val Asn Asn Thr	
395 400 405	
gaa agt tac atc cac aga aat tta cct aca ttg gaa gag tat gat tca	1303
Glu Ser Tyr Ile His Arg Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser	
410 415 420	
tac tgg tgg ctg ggt ggc ctg gtc atc tgc tct ctg ctg acc ctc atc	1351
Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys Ser Leu Leu Thr Leu Ile	
425 430 435	
gtg att ttt tac tac ctg ggc tta ctg tgt ggc gtg tgc ggc tat gac	1399
Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp	
440 445 450	
agg cat gcc acc ccg acc acc cga ggc tgt gtc tcc aac acc gga ggc	1447
Arg His Ala Thr Pro Thr Thr Arg Gly Cys Val Ser Asn Thr Gly Gly	
455 460 465 470	
gtc ttc ctc atg gtt gga gtt gga tta agt ttc ctc ttt tgc tgg ata	1495
Val Phe Leu Met Val Gly Val Gly Leu Ser Phe Leu Phe Cys Trp Ile	
475 480 485	
ttg atg atc att gtg gtt ctt acc ttt gtc ttt ggt gca aat gtg gaa	1543
Leu Met Ile Ile Val Val Leu Thr Phe Val Phe Gly Ala Asn Val Glu	
490 495 500	
aaa ctg atc tgt gaa cct tac acg agc aag gaa tta ttc cgg gtt ttg	1591
Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu	
505 510 515	
gat aca ccc tac tta cta aat gaa gac tgg gaa tac tat ctc tct ggg	1639
Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly	
520 525 530	
aag cta ttt aat aaa tca aaa atg aag ctc act ttt gaa caa gtt tac	1687
Lys Leu Phe Asn Lys Ser Lys Met Lys Leu Thr Phe Glu Gln Val Tyr	
535 540 545 550	
agt gac tgc aaa aaa aat aga ggc act tac ggc act ctt cac ctg cag	1735
Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr Gly Thr Leu His Leu Gln	
555 560 565	
aac agc ttc aat atc agt gaa cat ctc aac att aat gag cat act gga	1783

810

815

820

act ata ccc atg aaa aat atg gaa aat ggt aat aat ggt tat cat aaa 2551
 Thr Ile Pro Met Lys Asn Met Glu Asn Gly Asn Asn Gly Tyr His Lys
 825 830 835

gat cat gta tat ggt att cac aat cct gtt atg aca agc cca tca caa 2599
 Asp His Val Tyr Gly Ile His Asn Pro Val Met Thr Ser Pro Ser Gln
 840 845 850

cat tga tagctgatgt tgaaactgct tgagcatcag gataactcaaa gtggaaagga 2655
 His
 855

tcacagattt ttggtagttt ctgggtctac aaggactttc caaatccagg agcaacgcca 2715

gtggcaacgt agtgactcag gcgggcacca aggcaacggc accattgggtc tctgggtagt 2775

gctttaagaa tgaacacaat cacgttatag tccatgggtcc atcactattc aaggatgact 2835

ccctcccttc ctgtctattt ttgtttttta cttttttaca ctgagtttct atttagacac 2895

tacaacatat ggggtgtttg ttcccattgg atgcatttct atcaaaaactc tatcaaagt 2955

gatggctaga ttctaacata ttgcatgtg tggagtgtgc tgaacacaca ccagtttaca 3015

ggaaagatgc attttgtgta cagtaaacgg tgtatatacc ttttgttacc acagagtttt 3075

ttaaacaaat gagtattata ggactttctt ctaaatagagc taaataagtc accattgact 3135

tcttggtgct gttgaaaata atccattttc actaaaagtg tgtgaaacct acagcatatt 3195

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ccctaaattt gcatgaaagc acaaggtaaa tattcatttg cttcaggagt ttcatgttgg 3615

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ctgattcatt tgaataaaaa ggaacttgg 3764

<210> 4

<211> 855

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Leu Val Leu Gly Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn

Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys Ser Leu His Gln
260 265 270

Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val Lys Thr Ser Leu
275 280 285

Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His Pro Ser Ser Glu
290 295 300

Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu Asn Ser Asn Pro
305 310 315 320

Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu Asp Asn Val Asn
325 330 335

Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln Gln Gly Tyr Gln
340 345 350

Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln Thr Thr Thr Val
355 360 365

Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly Ser Asp Ile Asp
370 375 380

Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu Ser Ala Phe Ser
385 390 395 400

Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg Asn Leu Pro Thr
405 410 415

Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly Leu Val Ile Cys
420 425 430

Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu Gly Leu Leu Cys
435 440 445

Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr Thr Arg Gly Cys
450 455 460

Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly Val Gly Leu Ser
465 470 475 480

Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val Leu Thr Phe Val
485 490 495

Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro Tyr Thr Ser Lys
500 505 510

Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu Asn Glu Asp Trp
515 520 525

Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser Lys Met Lys Leu
530 535 540

Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn Arg Gly Thr Tyr
545 550 555 560

Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser Glu His Leu Asn
565 570 575

Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu Glu Ser Leu Lys
580 585 590

Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly Arg Lys Asn Leu
595 600 605

Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn Tyr Asp Ser Tyr
610 615 620

Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn Leu Leu Ser Phe
625 630 635 640

Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro Pro Gly Asn Leu
645 650 655

Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys Thr Ile His Gln
660 665 670

Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr Leu Tyr Gln Ser
675 680 685

Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu Glu Arg Val Thr
690 695 700

Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe Ile Thr Asn Asn
705 710 715 720

Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr Gly Arg Thr Ile
725 730 735

Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu Phe Ser Ile Ser
740 745 750

Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala Leu Asp Thr Ala
755 760 765

Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro Leu Asn Leu Phe
770 775 780

Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu Pro Ala Leu Ile
785 790 795 800

Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met Asp Ser Glu Asp
805 810 815

Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn Met Glu Asn Gly
820 825 830

Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile His Asn Pro Val
835 840 845

Met Thr Ser Pro Ser Gln His
850 855

<210> 5

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Extracellular cytokine receptor motif found in many species.

<220>

<221> UNSURE

<222> (3)..(3)

<223> "Xaa" at position 3 can be any amino acid.

<400> 5

Trp Ser Xaa Trp Ser
1 5